F1

SEQUENCE LISTING

(1) GENERAL INFORMATION:
    (i) APPLICANT: Goodman, Corey S.
                Kidd, Thomas
                Mitchell, Kevin
                Tear, Guy
   (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and
        Nucleic Acids
  (iii) NUMBER OF SEQUENCES: 13
   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
       (B) STREET: 75 DENISE DRIVE
       (C) CITY: HILLSBOROUGH
       (D) STATE: CALIFORNIA
       (E) COUNTRY: USA
       (F) ZIP: 94010
    (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER:
       (B) FILING DATE:
       (C) CLASSIFICATION:
 (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: OSMAN, RICHARD A
       (B) REGISTRATION NUMBER: 36,627
       (C) REFERENCE/DOCKET NUMBER: B98-006
   (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: (650) 343-4341
       (B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:
    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 4188 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: cDNA
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG     240
GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA     300
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AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC     720
ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG     780
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TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG   3600
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CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG   3720
CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG   3780
CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC   3840
CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG   3900
GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC   3960
AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG   4020
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GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC     4080
TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC     4140
GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA                  4188
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(2) INFORMATION FOR SEQ ID NO:2:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1395 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
1               5                   10                  15
Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
            20                  25                  30
Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
            35                  40                  45
Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
        50                  55                  60
Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
65                  70                  75                  80
Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
                85                  90                  95
Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
            100                 105                 110
Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
        115                 120                 125
Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
    130                 135                 140
His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
145                 150                 155                 160
Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
                165                 170                 175
Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
                180                 185                 190
Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
        195                 200                 205
Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
    210                 215                 220
Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
225                 230                 235                 240
Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
                245                 250                 255
Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
            260                 265                 270
Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
        275                 280                 285
Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
        290                 295                 300
Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
305                 310                 315                 320
Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
                325                 330                 335
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Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
            340             345               350
Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
            355             360               365
Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
    370             375             380
Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
385             390             395                     400
Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
            405             410               415
Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
            420             425               430
Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
            435             440               445
Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
    450             455             460
Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
465             470             475                     480
Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
            485             490               495
Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
            500             505               510
Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
            515             520               525
Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
            530             535               540
Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
545             550             555                     560
Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
            565             570               575
Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
            580             585               590
Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
            595             600               605
Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
    610             615             620
Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
625             630             635                     640
Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
            645             650               655
Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
            660             665               670
Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
            675             680               685
Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
    690             695             700
Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
705             710             715                     720
Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
            725             730               735
Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
            740             745               750
Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
    755             760             765
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Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
    770             775                 780
Trp Val Arg Trp Thr Pro Pro Ser Gln His His Asn Gly Asn Leu
785             790                 795                 800
Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
            805                 810                 815
Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
            820                 825                 830
Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
    835                 840                 845
Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
    850                 855                 860
Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
865             870                 875                 880
Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
            885                 890                 895
Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
            900                 905                 910
Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
    915                 920                 925
Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
    930                 935                 940
Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
945                 950                 955                 960
Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
            965                 970                 975
His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
            980                 985                 990
Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
    995                 1000                1005
Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
    1010                1015                1020
Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
1025                1030                1035                1040
Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys
            1045                1050                1055
Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
            1060                1065                1070
Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
    1075                1080                1085
Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
    1090                1095                1100
Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala
1105                1110                1115                1120
Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser
            1125                1130                1135
Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser
            1140                1145                1150
Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val
            1155                1160                1165
Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
    1170                1175                1180
Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
1185                1190                1195                1200
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Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
            1205                1210                1215
Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
            1220                1225                1230
Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
            1235                1240                1245
Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
            1250                1255                1260
Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
1265                1270                1275                1280
His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
                1285                1290                1295
Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
                1300                1305                1310
Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
            1315                1320                1325
His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
            1330                1335                1340
Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
1345                1350                1355                1360
Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
                1365                1370                1375
Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
            1380                1385                1390
Lys Asn Thr
        1395


(2) INFORMATION FOR SEQ ID NO:3:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4146 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
GGTGAAAATC CACGCATCAT CGAGCATCCC ATGGACACGA CGGTGCCAAA AAATGATCCA    60
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GCCAAAAACG AGTTTGGAGT GGCACGGTCC AGGAATGCAA CGTTGCAAGT GGCAGTTCTC    300
CGCGACGAAT TCCGTTTGGA GCCGGCAAAT ACCCGCGTGG CCCAAGGCGA GGTGGCCCTG    360
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GGACCCCAGA ATCAGACGGC GGTGGTGGGC AGCTCGGTGG TCTTCCAGTG CCGCATCGGA    660
GGCGATCCCC TGCCTGATGT CCTGTGGCGA CGCACTGCCT CCGGCGGCAA TATGCCACTG    720
CGTAAGTTTT CTTGGCTTCA TTCAGCTTCA GGTCGTGTGC ACGTACTTGA GGACCGCAGT    780
CTGAAGCTGG ACGACGTTAC TCTGGAGGAC ATGGGCGAGT ACACTTGCGA GGCGGACAAT    840
GCGGTGGGCG GCATCACGGC CACTGGCATC CTCACCGTTC ACGCTCCCCC CAAATTTGTG    900
ATACGCCCCA AGAATCAGCT GGTGGAGATC GGTGATGAAG TGCTGTTCGA GTGCCAAGCG    960
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CCCGGCTATC GGGATGGCCG CATGGAAGTG ACCCTGACGC CGAGGGGCG CTCGGTGCTC    1080
TCGATAGCTC GATTTGCCCG TGAGGATTCC GGAAAGGTGG TCACTTGCAA CGCCCTGAAC    1140
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GCGCGCAATG GAAACGGCTA CTGGCTGGAC TCCTCCACCG GCGGAATGGT GTGGCGTCCC      2940
TCGCCCGGCG GCGACTCGCT GGAGATGCAA AAGGATCACA TCGCCGACTA TGCGCCGGTC      3000
TGCGGTGCCC CCGGTTCTCC GGCCGGCGGT GGCACCTCTT CCGGTGGATC CGGTGGCGCG      3060
GGCAGCGGTG CCAGCGGCGG CGATGACATT CATGGAGGAC ACGGCAGCGA ACGCAATCAG      3120
CAGCGGTACG TGGGCGAGTA CTCCAACATA CCGACCGACT ATGCAGAGGT GTCCAGTTTT      3180
GGCAAGGCAC CCAGCGAGTA TGGTCGGCAT GGCAACGCCT CCCCGGCCCC TTATGCCACC      3240
TCTTCGATCC TGAGTCCCCA CCAGCAGCAA CAGCAGCAGC AGCCGCGTTA TCAACAGCGA      3300
CCAGTGCCCG GCTATGGGCT CCAGCGCCCA ATGCACCCAC ACTACCAGCA GCAGCAGCAT      3360
CAGCAGCAAC AGGCGCAGCA GACGCACCAG CAACACCAGG CTCTCCAGCA GCACCAGCAA      3420
CTGCCACCCA GCAACATCTA CCAGCAGATG TCCACCACCA GCGAGATATA CCCCACGAAC      3480
ACGGGTCCTT CGCGCTCTGT CTACTCTGAG CAGTATTACT ACCCCAAGGA CAAGCAGAGA      3540
CACATCCACA TCACCGAGAA CAAGCTGAGC AACTGCCACA CCTATGAGGC GGCTCCTGGC      3600
GCCAAGCAGT CCTCGCCGAT ATCCTCGCAG TTCGCCAGCG TGAGGCGGCA GCAGCTGCCG      3660
CCCAACTGCA GCATCGGCAG GGAAAGTGCC CGCTTCAAGG TGCTAAACAC GGATCAGGGC      3720
AAGAACCAGC AGAATCTCCT GGATCTCGAC GGCTCCTCGA TGTGCTACAA CGGTCTGGCA      3780
GACTCGGGCT GCGGTGGATC TCCCTCCCCG ATGGCCATGC TGATGTCGCA CGAGGACGAG      3840
CACGCGCTGT ACCACACGGC GGATGGGGAT CTGGACGACA TGGAACGACT GTACGTCAAG      3900
GTGGACGAGC AGCAGCCTCC ACAGCAGCAG CAGCAGCTGA TTCCCCTGGT CCCACAGCAT      3960
CCGGCGGAAG GTCACCTGCA GTCCTGGCGG AATCAGAGCA CGCGGAGCAG TCGGAAGAAC      4020
GGCCAGGAAT GCATCAAGGA ACCCAGCGAG TTGATCTACG CTCCGGGAAG CGTGGCCAGC      4080
GAACGGAGCC TCCTCAGCAA CTCGGGTAGC GGCACCAGCA GCCAGCCAGC TGGCCACAAT      4140
GTCTGA                                                                 4146
```

(2) INFORMATION FOR SEQ ID NO:4:
     (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1381 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
1               5               10              15
Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
            20              25              30
Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
        35              40              45
Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
    50              55              60
Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu
65              70              75              80
Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln
            85              90              95
Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg
            100             105             110
Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly
            115             120             125
Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn
    130             135             140
Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala
145             150             155             160
Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val
            165             170             175
Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val
            180             185             190
His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val
    195             200             205
Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu
    210             215             220
Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu
225             230             235             240
Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu
            245             250             255
Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly
            260             265             270
Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr
            275             280             285
Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys
    290             295             300
Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala
305             310             315             320
Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser
            325             330             335
Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu
            340             345             350
Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu
    355             360             365
Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser
    370             375             380
```

```
Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro
385             390             395                 400
Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys
            405             410             415
Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln
            420             425             430
Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu
        435             440             445
Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln
    450             455             460
Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn
465             470             475             480
Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn
            485             490             495
Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly
            500             505             510
Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr
        515             520             525
Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly
    530             535             540
Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala
545             550             555             560
Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu
            565             570             575
Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
        580             585             590
Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
    595             600             605
Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
    610             615             620
Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
625             630             635             640
Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
            645             650             655
Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Ile Val Asn Asn Pro
        660             665             670
Ala Pro Val Thr Ser Asn Thr Asn Pro Leu Leu Gly Ser Thr Ser Thr
    675             680             685
Ser Ala Ser Ala Ser Ala Ser Ala Ser Ala Leu Ile Ser Thr Lys Pro
    690             695             700
Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
705             710             715                 720
Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
            725             730             735
Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
            740             745             750
Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
        755             760             765
Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
    770             775             780
Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
785             790             795                 800
Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
            805             810             815
```

```
Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
            820                 825             830
Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
        835                 840             845
Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
        850                 855             860
Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
865             870                 875                 880
Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln
                885                 890                 895
Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu
            900                 905                 910
Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val
        915                 920                 925
Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr
        930                 935                 940
Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser
945                 950                 955                 960
Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met
                965                 970                 975
Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp
                980                 985                 990
His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala
            995                 1000                1005
Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala
    1010                1015                1020
Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln
1025                1030                1035                1040
Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu
                1045                1050                1055
Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn
                1060                1065                1070
Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln
        1075                1080                1085
Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly
        1090                1095                1100
Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His
1105                1110                1115                1120
Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln
                1125                1130                1135
Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr
            1140                1145                1150
Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr
            1155                1160                1165
Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile
    1170                1175                1180
Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly
·1185                1190                1195                1200
Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg
                1205                1210                1215
Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe
            1220                1225                1230
Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp
        1235                1240                1245
```

```
Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
    1250                1255                1260
Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
    1265                1270                1275                1280
His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
                1285                1290                1295
Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
                1300                1305                1310
Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
            1315                1320                1325
Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
    1330                1335                1340
Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
1345                1350                1355                1360
Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
                1365                1370                1375
Ala Gly His Asn Val
                1380
```

(2) INFORMATION FOR SEQ ID NO:5:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3894 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT    60
AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG   120
GTATCTAGGG GATCGCCAGC AACCCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC   180
ACATGGTACA AGGATGGACA GCCCGTAATC ACGAATAAGG AGCAAGTGAA CAGCCACCGG   240
ATTGTTCTCG ACACGGGATC CCTGTTTCTT CTGAAAGTGA ATAGTGGAAA AAACGGAAAA   300
GACAGCGATG CGGGAGCGTA CTATTGTGTG GCCAGCAACG AGCACGGAGA AGTGAAGTCG   360
AACGAAGGAT CGTTAAAATT GGCGATGCTT CGCGAAGACT TTCGAGTTCG GCCAAGAACA   420
GTTCAGGCTC TTGGTGGAGA GATGGCCGTT CTGGAATGCA GTCCGCCACG TGGATTCCCG   480
GAGCCGGTTG TGAGCTGGCG GAAAGACGAC AAAGAGCTCC GAATTCAAGA CATGCCACGA   540
TACACTCTAC ACTCTGACGG AAACCTCATC ATTGATCCGG TCGATCGAAG CGATTCTGGT   600
ACTTATCAGT GTGTTGCCAA CAACATGGTC GGAGAACGGG TGTCCAATCC CGCAAGATTG   660
AGTGTCTTTG AGAAACCAAA GTTTGAGCAA GAACCCAAGG ACATGACGGT CGACGTCGGA   720
GCCGCAGTGC TGTTTGATTG TCGTGTGACT GGAGATCCTC AACCACAAAT TACGTGGAAA   780
CGCAAAAATG AGCCGATGCC AGTTACACGT GCATACATTG CCAAGGATAA TCGGGGGTTG   840
AGAATCGAAA GAGTTCAACC ATCAGACGAA GGTGAATACG TTTGCTATGC ACGAAATCCA   900
GCGGGAACTC TTGAAGCATC TGCACATCTT CGTGTCCAGG CACCTCCATC CTTCCAGACA   960
AAACCAGCAG ACCAGTCAGT TCCAGCTGGA GGCACGGCAA CTTTTGAATG CACCTTGGTC  1020
GGTCAACCGA GTCCCGCCTA TTTTTGGAGC AAGGAAGGCC AACAGGATCT TCTTTTCCCA  1080
AGTTATGTGT CCGCTGATGG TAGAACGAAA GTTTCACCAA CTGGAACATT GACAATTGAG  1140
GAAGTTCGTC AAGTTGATGA GGGAGCTTAT GTGTGCGCTG GAATGAACTC GGCAGGAAGC  1200
TCGTTGAGCA AGGCAGCTTT GAAAGCAACA TTTGAAACCA AAGGCCGTGT CCAAAAAAAA  1260
AAGAGCAAAA TGGGCAAACA GAAACAAAAA AATGTTCAAT CAATTATCAA ATATTTAATT  1320
TCAGCCGTGA CCGGAAACAC ACCCGCCAAA CCACCACCAA CAATCGAGCA TGGTCATCAA  1380
AATCAGACCC TTATGGTTGG ATCATCAGCC ATCCTTCCAT GTCAGGCTAG CGGAAAACCA  1440
ACTCCAGGAA TATCATGGCT CAGGGATGGG CTACCTATTG ACATTACAGA TAGTCGTATC  1500
AGTCAACATT CAACGGGAAG TCTACATATT GCCGATTTAA AGAAACCTGA CACCGGAGTT  1560
TACACTTGCA TTGCGAAGAA CGAGGATGGA GAGTCAACAT GGTCGGCATC TCTGACTGTT  1620
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GAAGATCACA CTAGCAATGC ACAATTTGTT CGGATGCCGG ATCCATCGAA CTTCCCGTCT    1680
TCTCCAACGC AACCCATTAT TGTCAATGTC ACTGATACCG AAGTAGAGCT CCACTGGAAT    1740
GCTCCCTCCA CATCTGGCGC AGGACCAATC ACTGGTTATA TCATTCAGTA CTACAGTCCA    1800
GACCTCGGAC AGACGTGGTT TAACATTCCA GACTACGTGG CATCTACTGA ATATAGAATA    1860
AAGGGTCTGA AACCATCTCA CTCGTATATG TTTGTGATTC GAGCAGAAAA TGAGAAAGGT    1920
ATTGGAACGC CGAGTGTGTC GTCGGCTCTC GTTACCACTA GCAAGCCAGC AGCTCAAGTT    1980
GCGCTTTCTG ACAAGAACAA AATGGACATG GCCATCGCTG AGAAGAGACT CACTTCGGAA    2040
CAACTCATAA AACTCGAGGA AGTGAAGACT ATTAATTCTA CGGCCGTTCG TTTGTTCTGG    2100
AAGAAGAGGA AACTTGAAGA GCTGATTGAT GGTTACTACA TCAAGTGGAG AGGGCCTCCA    2160
AGAACCAATG ATAATCAATA CGTGAATGTG ACCAGCCCTA GCACCGAAAA CTATGTTGTT    2220
TCAAATTTAA TGCCATTCAC CAACTATGAG TTTTTCGTGA TTCCTTATCA TTCCGGAGTT    2280
CATAGTATTC ATGGAGCACC GAGTAATTCC ATGGACGTGT TGACCGCCGA AGCTCCACCT    2340
TCATTGCCAC CAGAGGATGT GCGAATCCGT ATGCTCAACC TGACCACTCT TCGTATCTCT    2400
TGGAAAGCAC CAAAAGCCGA CGGCATCAAC GGAATTCTCA AAGGATTCCA AATTGTTATT    2460
GTTGGTCAAG CGCCCAACAA CAATCGGAAC ATCACTACAA ACGAGAGAGC TGCCAGTGTT    2520
ACTCTGTTCC ATTTAGTGAC TGGAATGACG TATAAAATTC GTGTAGCGGC TAGAAGCAAT    2580
GGTGGAGTTG GAGTCTCACA TGGAACGAGT GAAGTCATCA TGAATCAAGA CACGCTGGAA    2640
AAACACCTTG CTGCTCAACA AGAAAACGAA TCATTTTTGT ATGGGCTGAT CAATAAATCT    2700
CATGTTCCTG TGATTGTCAT TGTTGCAATT CTGATTATTT TCGTAGTCAT CATTATAGCC    2760
TATTGTTACT GGAGGAATAG CAGAAACAGT GATGGAAAGG ATCGAAGTTT TATAAAGATC    2820
AATGATGGAA GTGTTCATAT GGCTTCGAAT AATCTTTGGG ATGTTGCACA AAATCCGAAT    2880
CAGAATCCAA TGTACAACAC TGCTGGAAGA ATGACTATGA ACAATAGAAA TGGCCAGGCT    2940
CTCTATTCGC TGACACCAAA TGCGCAAGAC TTTTTCAACA ATTGTGATGA CTACAGTGGA    3000
ACGATGCACA GACCAGGATC CGAGCATCAC TATCATTATG CTCAACTGAC TGGCGGACCT    3060
GGTAATGCGA TGTCTACTTT TTATGGAAAC CAATATCACG ATGATCCATC TCCATATGCC    3120
ACCACAACAC TGGTCCTGTC GAACCAACAA CCAGCTTGGC TCAATGACAA AATGCTTCGC    3180
GCGCCAGCAA TGCCAACAAA TCCCGTGCCA CCAGAGCCAC CGGCGCGATA TGCAGATCAT    3240
ACCGCTGGAA GACGATCTCG ATCGAGCCGT GCATCCGATG GGAGAGGAAC TCTGAATGGC    3300
GGACTCCATC ACCGGACTAG CGGAAGTCAA CGGTCGGATA GTCCACCTCA CACAGATGTG    3360
AGCTATGTTC AGCTTCACTC ATCCGATGGA ACTGGTAGTA GTAAGGAAAG AACTGGGGAG    3420
CGGAGAACAC CACCGAATAA GACTCTGATG GACTTTATTC CGCCACCACC TTCCAATCCA    3480
CCACCACCTG GAGGGCACGT TTATGACACA GCAACTAGGC GTCAGTTGAA TCGTGGAAGT    3540
ACTCCACGAG AAGACACCTA CGATTCGGTC AGTGACGGAG CTTTTGCTCG GGTTGATGTG    3600
AATGCAAGGC CAACGAGTCG GAATCGGAAT TTGGGAGGAA GGCCGCTGAA AGGGAAACGA    3660
GACGACGATA GTCAGCGGTC TTCGTTGATG ATGGACGATG ATGGTGGATC TTCTGAAGCT    3720
GACGGGGAGA ACTCTGAAGG AGACGTTCCG CGTGGAGGTG TTAGAAAAGC AGTTCCTCGA    3780
ATGGGTATCT CTGCAAGTAC GCTGGCTCAT AGTTGTTACG GGACAAACGG CACTGCTCAA    3840
CGATTCCGGT CAATTCCACG TAACAATGGA ATCGTCACAC AAGAACAAAC TTGA          3894
```

(2) INFORMATION FOR SEQ ID NO:6:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1297 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Tyr Tyr Leu Gly Phe Tyr His Thr His Thr His Thr His Thr Tyr
1               5               10              15
Ile Asn Phe Asp Lys Ile Pro Asn Ala Ser Asn Leu Ala Pro Val Ile
            20              25              30
Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr
        35              40              45
Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys
```

```
            50                      55                      60
Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg
65                      70                      75                      80
Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly
                85                      90                      95
Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser
                100                     105                     110
Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala
        115                     120                     125
Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu
        130                     135                     140
Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe Pro
145                     150                     155                     160
Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile Gln
                165                     170                     175
Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile Asp
                180                     185                     190
Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn Asn
                195                     200                     205
Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe Glu
        210                     215                     220
Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val Gly
225                     230                     235                     240
Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro Gln
                245                     250                     255
Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala Tyr
                260                     265                     270
Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro Ser
                275                     280                     285
Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr Leu
        290                     295                     300
Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln Thr
305                     310                     315                     320
Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe Glu
                325                     330                     335
Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys Glu
                340                     345                     350
Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly Arg
        355                     360                     365
Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg Gln
        370                     375                     380
Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly Ser
385                     390                     395                     400
Ser Leu Ser Lys Ala Ala Leu Lys Ala Thr Phe Glu Thr Lys Gly Arg
                405                     410                     415
Val Gln Lys Lys Lys Ser Lys Met Gly Lys Gln Lys Gln Lys Asn·Val
                420                     425                     430
Gln Ser Ile Ile Lys Tyr Leu Ile Ser Ala Val Thr Gly Asn Thr Pro
                435                     440                     445
Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln Asn Gln Thr Leu
        450                     455                     460
Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala Ser Gly Lys Pro
465                     470                     475                     480
Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro Ile Asp Ile Thr
```

```
                    485                   490                   495
Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu His Ile Ala Asp
                500                   505                   510
Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile Ala Lys Asn Glu
                515                   520                   525
Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val Glu Asp His Thr
                530                   535                   540
Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser Asn Phe Pro Ser
545                   550                   555                   560
Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp Thr Glu Val Glu
                565                   570                   575
Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly Pro Ile Thr Gly
                580                   585                   590
Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln Thr Trp Phe Asn
                595                   600                   605
Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile Lys Gly Leu Lys
                610                   615                   620
Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu Asn Glu Lys Gly
625                   630                   635                   640
Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr Thr Ser Lys Pro
                645                   650                   655
Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met Asp Met Ala Ile
                660                   665                   670
Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys Leu Glu Glu Val
                675                   680                   685
Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp Lys Lys Arg Lys
                690                   695                   700
Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp Arg Gly Pro Pro
705                   710                   715                   720
Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser Pro Ser Thr Glu
                725                   730                   735
Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn Tyr Glu Phe Phe
                740                   745                   750
Val Ile Pro Tyr His Ser Gly Val His Ser Ile His Gly Ala Pro Ser
                755                   760                   765
Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro
770                   775                   780
Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr Leu Arg Ile Ser
785                   790                   795                   800
Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile Leu Lys Gly Phe
                805                   810                   815
Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn Arg Asn Ile Thr
                820                   825                   830
Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His Leu Val Thr Gly
                835                   840                   845
Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn Gly Gly Val Gly
                850                   855                   860
Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln Asp Thr Leu Glu
865                   870                   875                   880
Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe Leu Tyr Gly Leu
                885                   890                   895
Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val Ala Ile Leu Ile
                900                   905                   910
Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp Arg Asn Ser Arg
```

```
                 915                   920                   925
       Asn Ser Asp Gly Lys Asp Arg Ser Phe Ile Lys Ile Asn Asp Gly Ser
           930                   935                   940
       Val His Met Ala Ser Asn Asn Leu Trp Asp Val Ala Gln Asn Pro Asn
       945                   950                   955                   960
       Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg
                     965                   970                   975
       Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe
                 980                   985                   990
       Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu
                 995                   1000                  1005
       His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met
           1010                  1015                  1020
       Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala
       1025                  1030                  1035                  1040
       Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp
                     1045                  1050                  1055
       Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu
                 1060                  1065                  1070
       Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser
                 1075                  1080                  1085
       Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His
           1090                  1095                  1100
       Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val
       1105                  1110                  1115                  1120
       Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu
                     1125                  1130                  1135
       Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe
                 1140                  1145                  1150
       Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Gly Gly His Val Tyr
                 1155                  1160                  1165
       Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu
           1170                  1175                  1180
       Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val
       1185                  1190                  1195                  1200
       Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu
                     1205                  1210                  1215
       Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp
                     1220                  1225                  1230
       Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp
                 1235                  1240                  1245
       Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser
                 1250                  1255                  1260
       Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln
       1265                  1270                  1275                  1280
       Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln
                     1285                  1290                  1295
       Thr
```

(2) INFORMATION FOR SEQ ID NO:7:
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 4956 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double

       (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT      60
CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC     120
GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT     180
CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA     240
AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA     300
TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG     360
TTGCTGCCGA GTGGATCTTT ATTTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT     420
GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG GAGAGGCTGT GAGCCACAAT     480
GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG     540
GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC     600
ACCATTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AGATGAAAG AATAACTATA      660
CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT     720
GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG     780
AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA     840
TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA     900
GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG     960
ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA    1020
GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG    1080
GTTGTTGCTT TGGGACGGAC TGTAACTTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA    1140
GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG    1200
TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA    1260
TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG    1320
GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT    1380
CCTGTGAATC AGACTGTAGC CGTGGATGGC ACTTTCGTCC TCAGCTGTGT GGCCACAGGC    1440
AGTCCAGTGC CCACCATTCT GTGGAGAAAG GATGGAGTCC TCGTTTCAAC CCAAGACTCT    1500
CGAATCAAAC AGTTGGAGAA TGGAGTACTG CAGATCCGAT ATGCTAAGCT GGGTGATACT    1560
GGTCGGTACA CCTGCATTGC ATCAACCCCC AGTGGTGAAG CAACATGGAG TGCTTACATT    1620
GAAGTTCAAG AATTTGGAGT TCCAGTTCAG CCTCCAAGAC CTACTGACCC AAATTTAATC    1680
CCTAGTGCCC CATCAAAACC TGAAGTGACA GATGTCAGCA GAAATACAGT CACATTATCG    1740
TGGCAACCAA ATTTGAATTC AGGAGCAACT CCAACATCTT ATATTATAGA AGCCTTCAGC    1800
CATGCATCTG GTAGCAGCTG GCAGACCGTA GCAGAGAATG TGAAAACAGA AACATCTGCC    1860
ATTAAAGGAC TCAAACCTAA TGCAATTTAC CTTTTCCTTG TGAGGGCAGC TAATGCATAT    1920
GGAATTAGTG ATCCAAGCCA AATATCAGAT CCAGTGAAAA CACAAGATGT CCTACCAACA    1980
AGTCAGGGGG TGGACCACAA GCAGGTCCAG AGAGAGCTGG GAAATGCTGT TCTGCACCTC    2040
CACAACCCCA CCGTCCTTTC TTCCTCTTCC ATCGAAGTGC ACTGGACAGT AGATCAACAG    2100
TCTCAGTATA TACAAGGATA TAAAATTCTC TATCGGCCAT CTGGAGCCAA CCACGGAGAA    2160
TCAGACTGGT TAGTTTTTGA AGTGAGGACG CCAGCCAAAA ACAGTGTGGT AATCCCTGAT    2220
CTCAGAAAGG GAGTCAACTA TGAAATTAAG GCTCGCCCTT TTTTAATGA ATTTCAAGGA     2280
GCAGATAGTG AAATCAAGTT TGCCAAAACC CTGGAAGAAG CACCCAGTGC CCCACCCCAA    2340
GGTGTAACTG TATCCAAGAA TGATGGAAAC GGAACTGCAA TTCTAGTTAG TTGGCAGCCA    2400
CCTCCAGAAG ACACTCAAAA TGGAATGGTC AAGAGTATA AGGTTTGGTG TCTGGGCAAT      2460
GAAACTCGAT ACCACATCAA CAAAACAGTG GATGGTTCCA CCTTTTCCGT GGTCATTCCC    2520
TTTCTTGTTC CTGGAATCCG ATACAGTGTG GAAGTGGCAG CCAGCACTGG GGCTGGGTCT    2580
GGGGTAAAGA GTGAGCCTCA GTTCATCCAG CTGGATGCCC ATGGAAACCC TGTGTCACCT    2640
GAGGACCAAG TCAGCCTCGC TCAGCAGATT TCAGATGTGG TGAAGCAGCC GGCCTTCATA    2700
GCAGGTATTG GAGCAGCCTG TTGGATCATC CTCATGGTCT TCAGCATCTG GCTTTATCGA    2760
CACCGCAAGA AGAGAAACGG ACTTACTAGT ACCTACGCGG TATCAGAAA AGTCCCGTCT     2820
TTTACCTTCA CACCAACAGT AACTTACCAG AGAGGAGGCG AAGCTGTCAG CAGTGGAGGG    2880
AGGCCTGGAC TTCTCAACAT CAGTGAACCT GCCGCGCAGC CATGGCTGGC AGACACGTGG    2940
CCTAATACTG GCAACAACCA CAATGACTGC TCCATCAGCT GCTGCACGGC AGGCAATGGA    3000
AACAGCGACA GCAACCTCAC TACCTACAGT CGCCCAGCTG ATTGTATAGC AAATTATAAC    3060
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AACCAACTGG ATAACAAACA AACAAATCTG ATGCTCCCTG AGTCAACTGT TTATGGTGAT    3120
GTGGACCTTA GTAACAAAAT CAATGAGATG AAAACCTTCA ATAGCCCAAA TCTGAAGGAT    3180
GGGCGTTTTG TCAATCCATC AGGGCAGCCT ACTCCTTACG CCACCACTCA GCTCATCCAG    3240
TCAAACCTCA GCAACAACAT GAACAATGGC AGCGGGGACT CTGGCGAGAA GCACTGGAAA    3300
CCACTGGGAC AGCAGAAACA AGAAGTGGCA CCAGTTCAGT ACAACATCGT GGAGCAAAAC    3360
AAGCTGAACA AAGATTATCG AGCAAATGAC ACAGTTCCTC CAACTATCCC ATACAACCAA    3420
TCATACGACC AGAACACAGG AGGATCCTAC AACAGCTCAG ACCGGGGCAG TAGTACATCT    3480
GGGAGTCAGG GGCACAAGAA AGGGGCAAGA ACACCCAAGG TACCAAAACA GGGTGGCATG    3540
AACTGGGCAG ACCTGCTTCC TCCTCCCCCA GCACATCCTC CTCCACACAG CAATAGCGAA    3600
GAGTACAACA TTTCTGTAGA TGAAAGCTAT GACCAAGAAA TGCCATGTCC CGTGCCACCA    3660
GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT    3720
CCCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT    3780
GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG    3840
GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA    3900
CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTTCAGGACC CCTGGTCTCA    3960
GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG    4020
ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTTGGG    4080
GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG    4140
GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCACTGAT    4200
GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA    4260
CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC    4320
ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA    4380
GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT    4440
CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCAATC CAAGACACAG    4500
CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA    4560
TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT    4620
GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG    4680
AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC    4740
CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT    4800
CCCAGTTCCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA    4860
AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTACTTG GAGGATATGA AAGAGGAGAA    4920
GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA                             4956
```

(2) INFORMATION FOR SEQ ID NO:8:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1651 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
1               5                   10                  15
Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
            20                  25                  30
Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
        35                  40                  45
Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu
    50                  55                  60
Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser
65                  70                  75                  80
Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr
                85                  90                  95
Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys
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                    100                   105                   110
Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe
        115                   120                   125
Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val
    130                   135                   140
Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn
145                   150                   155                   160
Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro
                165                   170                   175
Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln
            180                   185                   190
Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly
            195                   200                   205
Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys
    210                   215                   220
Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys
225                   230                   235                   240
Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu
                245                   250                   255
Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala
                260                   265                   270
Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp
    275                   280                   285
Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys
    290                   295                   300
Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val
305                   310                   315                   320
Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val
                325                   330                   335
Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His
            340                   345                   350
Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val
    355                   360                   365
Thr Phe Gln Cys Glu Ala Thr Gly Asn Pro Gln Pro Ala Ile Phe Trp
    370                   375                   380
Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr Gln Pro Pro Gln
385                   390                   395                   400
Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp Leu Thr Ile Thr
                405                   410                   415
Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys Gln Thr Leu Asn
                420                   425                   430
Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu Val Thr Asp Val
            435                   440                   445
Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly Pro Val Asn Gln
    450                   455                   460
Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys Val Ala Thr Gly
465                   470                   475                   480
Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly Val Leu Val Ser
            485                   490                   495
Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly Val Leu Gln Ile
            500                   505                   510
Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr Cys Ile Ala Ser
    515                   520                   525
Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile Glu Val Gln Glu
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            530                    535                    540
Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile
545                    550                    555                    560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr
                565                    570                    575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr
                580                    585                    590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln
                595                    600                    605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu
                610                    615                    620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr
625                    630                    635                    640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp
                645                    650                    655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu
                660                    665                    670
Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser
                675                    680                    685
Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile
                690                    695                    700
Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu
705                    710                    715                    720
Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val
                725                    730                    735
Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg
                740                    745                    750
Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala
                755                    760                    765
Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val
770                    775                    780
Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro
785                    790                    795                    800
Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp
                805                    810                    815
Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly
                820                    825                    830
Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr
                835                    840                    845
Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser
                850                    855                    860
Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn Pro Val Ser Pro
865                    870                    875                    880
Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp Val Val Lys Gln
                885                    890                    895
Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp Ile Ile Leu Met
                900                    905                    910
Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys Arg Asn Gly Leu
                915                    920                    925
Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Pro Ser Phe Thr Phe Thr
930                    935                    940
Pro Thr Val Thr Tyr Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly
945                    950                    955                    960
Arg Pro Gly Leu Leu Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu
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                     965                  970                  975
Ala Asp Thr Trp Pro Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile
         980                  985                  990
Ser Cys Cys Thr Ala Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr
         995                 1000                 1005
Tyr Ser Arg Pro Ala Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp
     1010                 1015                 1020
Asn Lys Gln Thr Asn Leu Met Leu Pro Glu Ser Thr Val Tyr Gly Asp
1025                 1030                 1035                 1040
Val Asp Leu Ser Asn Lys Ile Asn Glu Met Lys Thr Phe Asn Ser Pro
         1045                 1050                 1055
Asn Leu Lys Asp Gly Arg Phe Val Asn Pro Ser Gly Gln Pro Thr Pro
             1060                 1065                 1070
Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn Leu Ser Asn Asn Met Asn
         1075                 1080                 1085
Asn Gly Ser Gly Asp Ser Gly Glu Lys His Trp Lys Pro Leu Gly Gln
     1090                 1095                 1100
Gln Lys Gln Glu Val Ala Pro Val Gln Tyr Asn Ile Val Glu Gln Asn
1105                 1110                 1115                 1120
Lys Leu Asn Lys Asp Tyr Arg Ala Asn Asp Thr Val Pro Pro Thr Ile
             1125                 1130                 1135
Pro Tyr Asn Gln Ser Tyr Asp Gln Asn Thr Gly Gly Ser Tyr Asn Ser
         1140                 1145                 1150
Ser Asp Arg Gly Ser Ser Thr Ser Gly Ser Gln Gly His Lys Lys Gly
         1155                 1160                 1165
Ala Arg Thr Pro Lys Val Pro Lys Gln Gly Gly Met Asn Trp Ala Asp
     1170                 1175                 1180
Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro His Ser Asn Ser Glu
1185                 1190                 1195                 1200
Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys
             1205                 1210                 1215
Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu
             1220                 1225                 1230
Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser
         1235                 1240                 1245
Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr
         1250                 1255                 1260
Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu
1265                 1270                 1275                 1280
Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val
             1285                 1290                 1295
Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly
             1300                 1305                 1310
Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu
     1315                 1320                 1325
Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg
         1330                 1335                 1340
Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly
1345                 1350                 1355                 1360
Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser
             1365                 1370                 1375
Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser
         1380                 1385                 1390
Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala
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Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln
    1410   1415   1420
Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro
1425   1430   1435   1440
Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln
           1445   1450   1455
Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg
        1460   1465   1470
Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro
        1475   1480   1485
Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg
    1490   1495   1500
Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg
1505   1510   1515   1520
Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp
           1525   1530   1535
Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu
        1540   1545   1550
Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala
     1555   1560   1565
Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile
    1570   1575   1580
Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp
1585   1590   1595   1600
Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln
        1605   1610   1615
Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val
        1620   1625   1630
Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu
     1635   1640   1645
Thr Glu Ser
1650

(2) INFORMATION FOR SEQ ID NO:9:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1300 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: cDNA
   (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 855..1187
        (D) OTHER INFORMATION: /note= "N signifies gap in sequence"
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAACTAAAGG AAACCCACAG      60
CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAAA CCAACCCCAG     120
CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA     180
CGTTCCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA     240
AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA     300
GGCCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT     360
GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT     420
CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTTCTGAT     480
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ACTGGCACTT ATACTTGTGT GGCTACAAGT TCAAGTGGAG AGGCTTCCTG GAGTGCAGTG      540
CTGGATGTGA CAGAGTCTGG AGCAACAATC AGTAAAAACT ATGATTTAAG TGACCTGCCA      600
GGGCCACCAT CCAAACCGCA AGTCACTGAT GTTACTAAGA ACAGTGTCAC CTTGTCCTGG      660
CAGCCAGGTA CCCCTGGAAC CCTTCCAGCA AGTGCATATA TCATTGAGGC TTTCAGCCAA      720
TCAGTGAGCA ACAGCTGGCA GACCGTGGCA AACCATGTAA AGACCACCCT CTATACTGTA      780
AGAGGACTGC GGCCCAATAC AATCTACTTA TTCATGGTCA GAGCGATCAA CCCCAAGGTY      840
TCAGTGACCC AAGTNAAACC ACAGAAAAAC AATGGATCCA CTTGGGCCAA TGTCCCTCTA      900
CCTCCCCCCC CAGTCCAGCC CCTTCCTGGC ACGGAGCTGG AACACTATGC AGTGGAACAA      960
CAAGAAAATG GCTATGACAG TGATAGCTGG TGCCCACCAT TGCCAGTACA AACTTACTTA     1020
CACCAAGGTC TGGAAGATGA ACTGGAAGAA GATGATGATA GGGTCCCAAC ACCTCCTGTT     1080
CGAGGCGTGG CTTCTTCTCC TGCTATCTCC TTTGGACAGC AGTCCACTGC AACTCTTACT     1140
CCATCCCCAC GGGAAGAGAT GCAACCCATG CTGCAGGCTT CACCTNTTTA CCTCCTCTCA     1200
AAGACCTCGA CCTACCAGCC CATTTTCTAC TGACAGTAAC ACCAGTGCAG CCCTGAGTCA     1260
AAGTCAGAGG CCTCGGCCCA CTAAAAAACA CAAGGGAGGG                           1300
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(2) INFORMATION FOR SEQ ID NO:10:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 434 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 285..396
        (D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Gln Ile Val Ala Gln Gly Arg Thr Val Thr Phe Pro Cys Glu Thr Lys
1               5                   10                  15
Gly Asn Pro Gln Pro Ala Val Phe Trp Gln Lys Glu Gly Ser Gln Asn
            20                  25                  30
Leu Leu Phe Pro Asn Gln Pro Gln Gln Pro Asn Ser Arg Cys Ser Val
        35                  40                  45
Ser Pro Thr Gly Asp Leu Thr Ile Thr Asn Ile Gln Arg Ser Asp Ala
    50                  55                  60
Gly Tyr Tyr Ile Cys Gln Ala Leu Thr Val Ala Gly Ser Ile Leu Ala
65          70                  75                      80
Lys Ala Gln Leu Glu Val Thr Asp Val Leu Thr Asp Arg Pro Pro Pro
                85                  90                  95
Ile Ile Leu Gln Gly Pro Ala Asn Gln Thr Leu Ala Val Asp Gly Thr
                100                 105                 110
Ala Leu Leu Lys Cys Lys Ala Thr Gly Asp Pro Leu Pro Val Ile Ser
            115                 120                 125
Trp Leu Lys Glu Gly Phe Thr Phe Pro Gly Arg Asp Pro Arg Ala Thr
        130                 135                 140
Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys Asn Leu Arg Ile Ser Asp
145                 150                 155                 160
Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser Ser Ser Gly Glu Ala Ser
                165                 170                 175
Trp Ser Ala Val Leu Asp Val Thr Glu Ser Gly Ala Thr Ile Ser Lys
                180                 185                 190
Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro Pro Ser Lys Pro Gln Val
        195                 200                 205
Thr Asp Val Thr Lys Asn Ser Val Thr Leu Ser Trp Gln Pro Gly Thr
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        210                   215                   220
Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln
225                   230                   235                   240
Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr
                245                   250                   255
Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met
                260                   265                   270
Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln
                275                   280                   285
Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro
                290                   295                   300
Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln
305                   310                   315                   320
Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val
                325                   330                   335
Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp
                340                   345                   350
Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala
                355                   360                   365
Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg
                370                   375                   380
Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser
385                   390                   395                   400
Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser
                405                   410                   415
Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys
                420                   425                   430
Gly Gly
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(2) INFORMATION FOR SEQ ID NO:11:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 444 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GCCCAGGCAG TTGCTGCAGC TGCGGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG       60
CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT      120
GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG      180
CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCCT      240
CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA      300
CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC      360
AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG      420
CGAACAAATC CAAGTGACCC CAGA                                            444
```

(2) INFORMATION FOR SEQ ID NO:12:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 148 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala
1               5                   10                  15
Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser
            20                  25                  30
Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser
            35                  40                  45
Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln
    50                  55                  60
Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro
65                  70                  75                  80
Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala
            85                  90                  95
Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu
            100                 105                 110
Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly
            115                 120                 125
Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro
    130                 135                 140
Ser Asp Pro Arg
145

(2)  INFORMATION FOR SEQ ID NO:13:
     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 909 amino acids
          (B)  TYPE: amino acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear
     (ii)  MOLECULE TYPE: peptide
     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:13:
Met Phe Asn Arg Lys Thr Leu Leu Cys Thr Ile Leu Leu Val Leu Gln
1           .   5                   10                  15
Ala Val Ile Arg Ser Phe Cys Glu Asp Ala Ser Asn Leu Ala Pro Val
            20                  25                  30
Ile Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala
            35                  40                  45
Thr Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr
    50                  55                  60
Lys Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His
65                  70                  75                  80
Arg Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser
            85                  90                  95
Gly Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala
            100                 105                 110
Ser Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu
            115                 120                 125
Ala Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala
    130                 135                 140
Leu Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe
145                 150                 155                 160
Pro Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile
            165                 170                 175
Gln Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile
            180                 185                 190
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Asp Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn
        195   200   205
Asn Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe
        210   215   220
Glu Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val
225   230   235   240
Gly Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro
                245   250   255
Gln Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala
        260   265   270
Tyr Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro
        275   280   285
Ser Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr
        290   295   300
Leu Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln
305   310   315   320
Thr Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe
                325   330   335
Glu Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys
        340   345   350
Glu Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly
        355   360   365
Arg Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg
        370   375   380
Gln Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly
385   390   395   400
Ser Ser Leu Ser Lys Ala Ala Leu Lys Val Thr Thr Lys Ala Val Thr
                405   410   415
Gly Asn Thr Pro Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln
                420   425   430
Asn Gln Thr Leu Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala
        435   440   445
Ser Gly Lys Pro Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro
450   455   460
Ile Asp Ile Thr Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu
465   470   475   480
His Ile Ala Asp Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile
                485   490   495
Ala Lys Asn Glu Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val
        500   505   510
Glu Asp His Thr Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser
        515   520   525
Asn Phe Pro Ser Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp
        530   535   540
Thr Glu Val Glu Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly
545   550   555   560
Pro Ile Thr Gly Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln
                565   570   575
Thr Trp Phe Asn Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile
                580   585   590
Lys Gly Leu Lys Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu
        595   600   605
Asn Glu Lys Gly Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr
        610   615   620

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Thr Ser Lys Pro Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met
625             630             635                 640
Asp Met Ala Ile Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys
            645             650                 655
Leu Glu Glu Val Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp
            660             665             670
Lys Lys Arg Lys Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp
            675             680             685
Arg Gly Pro Pro Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser
    690             695             700
Pro Ser Thr Glu Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn
705             710             715                 720
Tyr Glu Phe Phe Val Ile Pro Tyr His Ser Gly Val His Ser Ile His
            725             730             735
Gly Ala Pro Ser Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro
            740             745             750
Ser Leu Pro Pro Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr
            755             760             765
Leu Arg Ile Ser Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile
    770             775             780
Leu Lys Gly Phe Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn
785             790             795                 800
Arg Asn Ile Thr Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His
            805             810             815
Leu Val Thr Gly Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn
            820             825             830
Gly Gly Val Gly Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln
            835             840             845
Asp Thr Leu Glu Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe
    850             855             860
Leu Tyr Gly Leu Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val
865             870             875                 880
Ala Ile Leu Ile Ile Phe Val Val Ile Ile Ala Tyr Cys Tyr Trp
            885             890             895
Arg Asn Ser Arg Asn Ser Asp Gly Lys Asp Arg Ser Phe
    900             905
```